

SEQUENCE LISTING

<110> Juridical Foundation, Japanese Foundation For Cancer Research

<120> vector for gene therapy of malignant melanoma, with use of virus having MSH fused protein.

<130> H11-0241J2

<160> 39

<170> PatentIn Ver. 2.0

<210> 1

<211> 166

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a part of adenovirus type 5 fiber, AS linker peptide and  $\alpha$ -MSH.

<220>

<221> CDS

<222> (3).. (113)

<400> 1

gg gaa ttc tcg agt tac act ttt tca tac att gcc caa gaa cca tca 47

Glu Phe Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu Pro Ser

1 5 10 15

gcc tcc gca tct gct tcc gcc cct gga tcc tac tcc atg gag cac ttc 95

Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Tyr Ser Met Glu His Phe

20 25 30

cgc tgg ggc aag ccg gtg taaagaatcg tttgtgttat gtttcaacgt 143

Arg Trp Gly Lys Pro Val

35

gtttatTTTT caattgaatt ccc 166

<210> 2

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 924 used as template for PCR amplification of DNA sequence No. 1.

<400> 2

cgttgaaaca taacacaaac gattcitttac accggcttgc cccagcggaa gtgctccatg 60

gagtaggatac caggggcgga agcagatgcg gaggctgatg gticttgggc aatgtatgaa 120

aaagtg 126

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 933 used as sense primer for PCR amplification of DNA sequence No. 1.

<400> 3

gggaattctc gagttacact tttcataca ttgcccaag

39

<210> 4

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 934 used as antisense primer for PCR amplification of DNA sequence No. 1.

<400> 4

gggaattcaa ttgaaaaata aacacgttga aacataacac aaacgattc

49

<210> 5

<211> 76

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1061 used as sense primer for PCR amplification of DNA coding  $\alpha$ -MSH and adenovirus fiber poly A signal.

<400> 5

cgggatccta ctccatggag cacttccgct ggggcaagcc ggtgtaagtc gacaagaata 60  
aagaatcggt tgtgtt 76

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1092 used as antisense primer for PCR amplification of DNA coding  $\alpha$ -MSH and adenovirus fiber poly A signal.

<400> 6

cggaattcat ggcgccaatgt ttaatcagag gt 32

<210> 7

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asMSHa

<220>

<221> CDS

<222> (1)..(1815)

<400> 7

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45



Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528  
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576  
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624  
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672  
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720  
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768  
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255



Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
 385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248  
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296  
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344  
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
 435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392  
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
 450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440  
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga 1776

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

580

585

590

tcc tac tcc atg gag cac ttc cgc tgg ggc aag ccg gtg taa 1818

Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val

595

600

605

<210> 8

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1037 used as sense primer for PCR amplification of  
DNA coding human MSH receptor residue 1-154.

<400> 8

gggaattcac catggctigc cagggatccc agagaagact

40

<210> 9

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1038 used as antisense primer for PCR amplification of DNA coding human MSH receptor residue 150-317.

<400> 9

gggaattcac caggagcatg tcagcacctc ctt

33

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1039 used as sense primer for PCR amplification of DNA coding human MSH receptor residue 150-317.

<400> 10

ctgcggtacc acagcatcgt gaccctg

27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1040 used as antisense primer for PCR amplification of DNA coding human MSH receptor residue 1-154.

<400> 11

gctgtgttac cgcagtgctt agaagat

27

<210> 12

<211> 107

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1075 used as sense primer for PCR amplification of DNA coding  $\beta$ -MSH and adenovirus fiber poly A signal.

<400> 12

cgcggaatccg ccgagaagaa ggacgagggc ccctacagga tggagcactt ccgctggggc

60

agccccccca aggactaagt cgacaagaat aaagaatcgt ttgtgtt

107

<210> 13

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asMSHb

<220>

<221> CDS

<222> (1)..(1845)

<400> 13

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528  
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

270

285

300

320

335

350

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat icc ttc ctg gac cca gaa tat tgg aac ttt 1440

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545 550 555 560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565 570 575

tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga 1776  
 Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

580

585

590

tcc gcc gag aag aag gac gag ggc ccc tac agg atg gag cac ttc cgc 1824  
 Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg

595

600

605

tgg ggc agc ccg ccc aag gac taa 1848  
 Trp Gly Ser Pro Pro Lys Asp

610

615

<210> 14

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1060 used as antisense primer for PCR amplification  
 of DNA coding a part of adenovirus type 5 fiber and GS linker peptide.

<400> 14

cgggatccag atccagaacc actaccactt ccagaacctt cttgggcaat gtatgaaaaa 60

g

61

<210> 15

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1098 used as antisense primer for PCR amplification of DNA coding a part of adenovirus type 5 fiber and GS linker peptide.

<400> 15

cgtgtggatc cgctgccaga accactacca cttccagaac c

41

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 931 used as sense primer for PCR amplification of DNA coding a part of adenovirus type 5 fiber and GS linker peptide.

<400> 16

ggcctttact tgtttiacagc

20

<210> 17

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6. 7R-F/gsMSHa

<220>

<221> CDS

<222> (1).. (1815)

<400> 17

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

tig cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192



aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528  
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 1008  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 1056  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 1104  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
 385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248  
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296  
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344  
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
 435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392  
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
 450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728  
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575

tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga 1776  
 Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly  
 580 585 590

tcc tac tcc atg gag cac ttc cgc tgg ggc aag ccg gtg taa 1818  
 Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val  
 595 600 605

<210> 18

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/gSMShb

<220>

<221> CDS

<222> (1).. (1845)

<400> 18

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48  
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
 1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96  
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
 20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144  
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192  
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
 50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 1008

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 1056

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 1104

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344  
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
 435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392  
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
 450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440  
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga 1776

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

580

585

590

tcc gcc gag aag aag gac gag ggc ccc tac agg atg gag cac ttc cgc 1824

Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg

595

600

605

tgg ggc agc ccg ccc aag gac taa

1848

Trp Gly Ser Pro Pro Lys Asp

610

615

<210> 19

<211> 128

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA No. 1089 used as sense primer for PCR amplification of DNA coding K21 linker peptide.

<400> 19

ccggaattca gatctggatc taagaagaag aagaagaaaa agaagaaaaa gaagaagaag 60  
aaaaaaaaaga agaagaaaaa gaaaggatcc taagatatcg tcgacaagaa taaagaatcg 120  
tttgtgtt 128

<210> 20

<211> 1893

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asK21MSHa

<220>

<221> CDS

<222> (1).. (1890)

<400> 20



100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

[illegible]

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248  
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga 1776

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

580

585

590

tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag 1824

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

595

600

605

aaa aaa aag aag aag aaa aag aaa gga tcc tac tcc atg gag cac ttc 1872

Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe

610

615

620

cgc tgg ggc aag ccg gtg taa

1893

Arg Trp Gly Lys Pro Val

625

630

<210> 21

<211> 1893

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/gsK21MSHa

<220>

<221> CDS

<222> (1)..(1890)

<400> 21

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240  
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288  
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336  
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384  
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432  
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gti act 720

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 1008

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 1056

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 1104

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392  
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440  
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly



<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6.7R-F/asK21MSHb

<220>

<221> CDS

<222> (1)..(1920)

<400> 22

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

tig cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384  
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528  
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576  
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624  
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672  
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225                      230                      235                      240

Gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768  
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

255

Gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816  
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 1008

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 1056

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 1104

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488  
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536  
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728  
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575

tac att gcc caa gaa cca tca gcc tcc gca tct gct tcc gcc cct gga 1776

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

580

585

590

tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag 1824

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

595

600

605

aaa aaa aag aag aag aaa aag aaa gga tcc gcc gag aag aag gac gag 1872

Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu

610

615

620

ggc ccc tac agg atg gag cac ttc cgc tgg ggc agc ccg ccc aag gac 1920

Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp

625

630

635

640

taa

1923

<210> 23

<211> 1923

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding a modified fiber protein of pWE6. 7R-F/gsK21MSHb

<220>

<221> CDS

<222> (1).. (1920)

<400> 23

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 480

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

57/107

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 1008

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 1056

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 1104

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 1152

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 1248

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 1296

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 1344

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 1392

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 1440

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 1488

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 1536

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc acc tcg agt tac act ttt tca 1728

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa ggt tct gga agt ggt agt ggt tct ggc agc gga 1776

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

580

585

590

tct gga tct aag aag aag aag aag aaa aag aag aaa aag aag aag aag 1824

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

595

600

605

61/107

aaa aaa aag aag aag aaa aag aaa gga tcc gcc gag aag aag gac gag 1872

Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu

610

615

620

ggc ccc tac agg atg gag cac ttc cgc tgg ggc agc ccg ccc aag gac 1920

Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp

625

630

635

640

taa

1923

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding AS linker

<220>

<221> CDS

<222> (1).. (33)

<400> 24

cca tca gcc tcc gca tct gct tcc gcc cct gga

33

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

1

5

10

<210> 25

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS linker peptide

<400> 25

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

1

5

10

<210> 26

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding GS linker

<220>

<221> CDS

<222> (1).. (33)

<400> 26

ggt tct gga agt ggt agt ggt tct ggc agc gga

33

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

1

5

10

<210> 27

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> GS linker peptide

<400> 27

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

1

5

10

<210> 28

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding ask21 linker

<220>

<221> CDS

<222> (1).. (108)

<400> 28

cca tca gcc tcc gca tct gct tcc gcc cct gga tct gga tct aag aag 48

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Gly Ser Lys Lys

1 5 10 15

aag aag aag aaa aag aag aaa aag aag aag aag aaa aaa aag aag aag 96

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

20 25 30

aaa aag aaa gga

108

Lys Lys Lys Gly

35

<210> 29

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> asK21 linker peptide

<400> 29

Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly Ser Gly Ser Lys Lys  
1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
20 25 30

Lys Lys Lys Gly  
35

<210> 30

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA coding gsK21 linker

<220>

<221> CDS

<222> (1).. (108)

<400> 30

ggt tct gga agt ggt agt ggt tct ggc agc gga tct gga tct aag aag 48  
 Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Lys Lys  
 1 5 10 15

aag aag aag aaa aag aag aaa aag aag aag aag aaa aaa aag aag aag 96  
 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
 20 25 30

aaa aag aaa gga 108  
 Lys Lys Lys Gly  
 35

<210> 31

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> gsK21 linker peptide

<400> 31

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Lys Lys  
 1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

20

25

30

Lys Lys Lys Gly

35

&lt;210&gt; 32

&lt;211&gt; 605

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; a modified fiber protein encoded in pWE6.7R-F/asMSHa

&lt;400&gt; 32

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
 1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
 20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
565 570 575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Pro Gly  
580 585 590

Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val  
595 600 605

<210> 33

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/asMSHb

<400> 33

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
565 570 575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly  
580 585 590

Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg  
595 600 605

Trp Gly Ser Pro Pro Lys Asp  
610 615

<210> 34

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/gsMSHa

<400> 34

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly

580

585

590

Ser Tyr Ser Met Glu His Phe Arg Trp Gly Lys Pro Val

595

600

605

<210> 35

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/gsMSHb

<400> 35

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305

310

315

320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325

330

335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340

345

350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355

360

365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370

375

380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385

390

395

400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly

580

585

590

Ser Ala Glu Lys Lys Asp Glu Gly Pro Tyr Arg Met Glu His Phe Arg

595

600

605

Trp Gly Ser Pro Pro Lys Asp

610

615

<210> 36

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/ask21MSHa

<400> 36

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Ser Ala Pro Gly

580

585

590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys

595

600

605

Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe

610

615

620

Arg Trp Gly Lys Pro Val

625

630

<210> 37

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6. 7R-F/gsK21MSHa

<400> 37

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

Tyr Ile Ala Gln Glu Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly  
580 585 590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
595 600 605

Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Tyr Ser Met Glu His Phe  
610 615 620

Arg Trp Gly Lys Pro Val  
625 630

<210> 38

<211> 640

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6. 7R-F/asK21MSHb

<400> 38

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

Tyr Ile Ala Gln Glu Pro Ser Ala Ser Ala Ser Ala Pro Gly  
580 585 590

Ser Gly Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
595 600 605

Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Ser Ala Glu Lys Lys Asp Glu  
610 615 620

Gly Pro Tyr Arg Met Glu His Phe Arg Trp Gly Ser Pro Pro Lys Asp  
625 630 635 640

<210> 39

<211> 640

<212> PRT

<213> Artificial Sequence

<220>

<223> a modified fiber protein encoded in pWE6.7R-F/gSK21MSHb

<400> 39

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65

70

75

80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

85

90

95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

100

105

110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

115

120

125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

130

135

140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145

150

155

160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

165

170

175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

275

280

285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

590

605

620

640